

BRUNOVSKIS

Page 1 of 7

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1632

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/051,034A

DATE: 11/20/2000
TIME: 12:18:27

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3 <110> APPLICANT: MCKENZIE, IAN FARQUHAR CAMPBELL
4 SANDRIN, MAURO SERGIO
5 <120> TITLE OF INVENTION: IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC
6 GLYCOSYLTRANSFERASE
9 <130> FILE REFERENCE: 30562.6USWO
11 <140> CURRENT APPLICATION NUMBER: 09/051,034A
12 <141> CURRENT FILING DATE: 1998-03-31
14 <150> PRIOR APPLICATION NUMBER: PCT/AU97/00492
15 <151> PRIOR FILING DATE: 1997-08-01
17 <150> PRIOR APPLICATION NUMBER: 60/024,279
18 <151> PRIOR FILING DATE: 1996-08-21
20 <150> PRIOR APPLICATION NUMBER: P01402
21 <151> PRIOR FILING DATE: 1996-08-02
23 <160> NUMBER OF SEQ ID NOS: 14
25 <170> SOFTWARE: PatentIn Ver. 2.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1043
29 <212> TYPE: DNA
30 <213> ORGANISM: Sus Domesticus
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33 <221> NAME/KEY: CDS
34 <222> LOCATION: (9)..(1031)
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39 1 5 10
41 ttc atc ctc ttt gtc ttc acg gct tcc acc ata ttt cac ctt cag cag 98
42 Phe Ile Leu Phe Val Phe Thr Ala Ser Thr Ile Phe His Leu Gln Gln
43 15 20 25 30
45 agg atg gtg aag att caa ccc acg tgg gag tta cag atg gtg acg cag 146
46 Arg Met Val Lys Ile Gln Pro Thr Trp Glu Leu Gln Met Val Thr Gln
47 35 40 45
49 gtg acc aca gag agc ccc tgg acg ccc cag ctg aag ggc atg tgg acg 194
50 Val Thr Thr Glu Ser Pro Ser Ser Pro Gln Leu Lys Gly Met Trp Thr
51 50 55 60
53 atc aat gcc atc ggc cgc ctg ggg aac cag atg ggg gag tac gcc acc 242
54 Ile Asn Ala Ile Gly Arg Leu Gly Asn Gln Met Gly Glu Tyr Ala Thr
55 65 70 75
57 ctg tac gcg ctg gcc agg atg aac ggg cgg ccc gtc atc ccc 290
58 Leu Tyr Ala Leu Ala Arg Met Asn Gly Arg Pro Ala Phe Ile Pro Pro
59 80 85 90
61 gag atg cac agc acg ctg gcc ccc atc ttc agg atc acc ctc ccc gtc 338
62 Glu Met His Ser Thr Leu Ala Pro Ile Phe Arg Ile Thr Leu Pro Val
63 95 100 105 110
65 ctg cac gcc agc acg gcc cgc agg atc ccc tgg cag aac tac cac ctg 386
66 Leu His Ala Ser Thr Ala Arg Arg Ile Pro Trp Gln Asn Tyr His Leu
67 115 120 125

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70	Asn	Asp	Irp	Met	Glu	Glu	Arg	Tyr	Arg	His	Ile	Pro	Gly	Glu	Tyr	Val	
71				130						135					140		
73	cgc	ctc	acg	ggc	tac	ccc	tgc	tcc	tgg	acc	ttc	tac	cac	cac	ctg	cgc	482
74	Arg	Leu	Thr	Gly	Tyr	Pro	Cys	Ser	Irp	Thr	Phe	Tyr	His	His	Leu	Arg	
75					145					150				155			
77	acc	gag	atc	ctc	cgg	gag	ttc	acc	ctg	cac	ttt	cgc	qag	gag		530	
78	Thr	Glu	Ile	Leu	Arg	Glu	Phe	Thr	Leu	His	Asn	His	Val	Arg	Glu	Glu	
79					160				165				170				
81	gcc	cag	gat	ttc	ctg	cg	gg	ctg	cg	gg	acc	ggg	agc	cga	ccg	agt	578
82	Ala	Gln	Asp	Phe	Leu	Arg	Gly	Leu	Arg	Val	Asn	Gly	Ser	Arg	Pro	Ser	
83	175				180				185				190				
85	acc	tac	gtg	ggg	gtg	cac	gtg	cgc	ggg	gac	tac	gtg	cac	gtg	atg	626	
86	Thr	Tyr	Val	Gly	Val	His	Val	Arg	Arg	Gly	Asp	Tyr	Val	His	Val	Met	
87					195				200				205				
89	ccc	aac	gtg	tgg	aaq	ggc	gtg	gtg	gcc	gac	cg	gg	tac	ctg	qag	cag	674
90	Pro	Asn	Val	Trp	Lys	Gly	Val	Val	Ala	Asp	Arg	Arg	Tyr	Leu	Gln		
91					210				215				220				
93	gcc	ctg	gac	tgg	ttc	cg	gg	ct	cgc	tac	ccc	gtc	ttt	gtg	gtc	722	
94	Ala	Leu	Asp	Trp	Phe	Arg	Ala	Arg	Tyr	Arg	Ser	Pro	Val	Phe	Val	Val	
95					225				230				235				
97	tcc	agc	aac	ggc	atg	gcc	tgg	tgt	cg	gaa	aac	atc	aat	gcc	tcg	cgc	770
98	Ser	Ser	Asn	Gly	Met	Ala	Trp	Cys	Arg	Glu	Asn	Ile	Asn	Ala	Ser	Arg	
99					240				245				250				
101	qgc	gat	gtg	gtg	ttt	gcc	ggc	aat	ggc	atc	gaq	ggc	tcc	ccc	gcc	aaa	818
102	Gly	Asp	Val	Val	Phe	Ala	Gly	Asn	Gly	Ile	Glu	Gly	Ser	Pro	Ala	Lys	
103	255				260				265				270				
105	gac	ttc	g	cg	ctg	ctc	acg	ca	g	tac	act	gtc	atg	acc	att	ggc	866
106	Asp	Phe	Ala	Leu	Leu	Thr	Gly	Cys	Asn	His	Thr	Val	Met	Thr	Ile	Gly	
107					275				280				285				
109	acg	tcc	ggg	atc	tgg	ggc	gcc	tac	ctt	gtc	gg	gag	acc	atc	tac	914	
110	Thr	Phe	Gly	Ile	Trp	Ala	Ala	Tyr	Leu	Ala	Gly	Gly	Ile	Thr	Ile	Tyr	
111					290				295				300				
113	ctg	gcc	aat	tac	acg	ctc	ccg	gac	tct	ccc	tcc	aaa	ctc	ttt	aag	962	
114	Leu	Ala	Asn	Tyr	Thr	Leu	Pro	Asp	Ser	Pro	Phe	Leu	Lys	Leu	Phe	Lys	
115					305				310				315				
117	ccc	gag	gca	gcc	ttc	ctg	ccc	gag	tgg	att	ggg	atc	gag	gca	gac	ctg	1010
118	Pro	Glu	Ala	Ala	Phe	Leu	Pro	Glu	Trp	Ile	Gly	Ile	Glu	Ala	Asp	Leu	
119					320				325				330				
121	tcc	cca	ctc	ctt	aag	cac	tga	tgt	cg	gt	cc					1043	
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134 Leu Phe Val Phe Thr Ala Ser Thr Ile Phe His Leu Gln Gln Arg Met
 135 20 25 30
 136 Val Lys Ile Gln Pro Thr Irp Glu Leu Gln Met Val Thr Gln Val Thr
 137 35 40 45
 138 Thr Glu Ser Pro Ser Ser Pro Gln Leu Lys Gly Met Trp Thr Ile Asn
 139 50 55 60
 140 Ala Ile Gly Arg Leu Gly Asn Gln Met Gly Glu Tyr Ala Thr Leu Iyr
 141 65 70 75 80
 142 Ala Leu Ala Arg Met Asn Gly Arg Pro Ala Phe Ile Pro Pro Glu Met
 143 85 90 95
 144 His Ser Thr Leu Ala Pro Ile Phe Arg Ile Thr Leu Pro Val Leu His
 145 100 105 110
 146 Ala Ser Thr Ala Arg Arg Ile Pro Trp Gln Asn Tyr His Leu Asn Asp
 147 115 120 125
 148 Trp Met Glu Glu Arg Tyr Arg His Ile Pro Gly Glu Tyr Val Arg Leu
 149 130 135 140
 150 Thr Gly Tyr Pro Cys Ser Trp Thr Phe Tyr His His Leu Arg Thr Glu
 151 145 150 155 160
 152 Ile Leu Arg Glu Phe Thr Leu His Asn His Val Arg Glu Glu Ala Gln
 153 165 170 175
 154 Asp Phe Leu Arg Gly Leu Arg Val Asn Gly Ser Arg Pro Ser Thr Tyr
 155 180 185 190
 156 Val Gly Val His Val Arg Arg Gly Asp Tyr Val His Val Met Pro Asn
 157 195 200 205
 158 Val Trp Lys Gly Val Val Ala Asp Arg Arg Iyr Leu Glu Gln Ala Leu
 159 210 215 220
 160 Asp Trp Phe Arg Ala Arg Tyr Arg Ser Pro Val Phe Val Val Ser Ser
 161 225 230 235 240
 162 Asn Gly Met Ala Trp Cys Arg Glu Asn Ile Asn Ala Ser Arg Gly Asp
 163 245 250 255
 164 Val Val Phe Ala Gly Asn Gly Ile Glu Gly Ser Pro Ala Lys Asp Phe
 165 260 265 270
 166 Ala Leu Leu Thr Gln Cys Asn His Thr Val Met Thr Ile Gly Thr Phe
 167 275 280 285
 168 Gly Ile Trp Ala Ala Tyr Leu Ala Gly Gly Glu Thr Ile Tyr Leu Ala
 169 290 295 300
 170 Asn Tyr Thr Leu Pro Asp Ser Pro Phe Leu Lys Leu Phe Lys Pro Glu
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 173 325 330 335
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 184 <220> FEATURE:
 185 <221> NAME/KEY: CDS
 186 <222> LOCATION: (1)..(1098)

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 191 1 5 10 15
 192 ttt gtt tta gca gca att ttc ttc ctg aac gtc tat caa gac ctc ttt 96
 193 Cys Val Leu Ala Ala Ile Phe Phe Leu Asn Val Tyr Gln Asp Leu Phe
 194 20 25 30
 195 tac agt ggc tta gac ctg ctg gcc ctg ttt cca gac cat aac gtc gta 144
 196 Tyr Ser Gly Leu Asp Leu Leu Ala Leu Cys Pro Asp His Asn Val Val
 197 35 40 45
 198 tca tct ccc gtc gtc gac ata ttc tgc ctg gtc ggc acg ccg gta cac ccc 192
 199 Ser Ser Pro Val Ala Ile Phe Cys Leu Ala Gly Thr Pro Val His Pro
 200 50 55 60
 201 aac qcc tcc gat tcc ttt ccc aac cat cct gcc tcc ttt tcc ggg acc 240
 202 Asn Ala Ser Asp Ser Cys Pro Lys His Pro Ala Ser Phe Ser Gly Thr
 203 65 70 75 80
 204 tgg act att tac ccc gat ggc cgg ttt ggg aac cag atg gga caq tat 288
 205 Itp Thr Ile Tyr Pro Asp Gly Arg Phe Gly Asn Gln Met Gly Gln Tyr
 206 85 90 95
 207 qcc acq ctg ctg gcc ctg gtc cag ctc aac ggc cgc cag gcc ttc atc 336
 208 Ala Thr Leu Leu Ala Leu Ala Gln Leu Asn Gly Arg Gln Ala Phe Ile
 209 100 105 110
 210 cag cct gcc atg cac gtc ctg gcc ccc gtc ttc cgc atc acq ctg 384
 211 Gln Pro Ala Met His Ala Val Leu Ala Pro Val Phe Arg Ile Thr Leu
 212 115 120 125
 213 cct gtc ctg gtc ccc gag gta gac agg cac gct cct tgg cgg gag ctg 432
 214 Pro Val Leu Ala Pro Glu Val Asp Arg His Ala Pro Trp Arg Glu Leu
 215 130 135 140
 216 gag ctt cac gac tgg atg tcc gag gat tat gcc cac tta aag gag ccc 480
 217 Glu Leu His Asp Trp Met Ser Glu Asp Tyr Ala His Leu Lys Glu Pro
 218 145 150 155 160
 219 tgg ctg aag ctc acc qcc ttc ccc tcc tcc tgg acc ttc ttc cac cac 528
 220 Trp Leu Lys Leu Thr Gly Phe Pro Cys Ser Trp Thr Phe Phe His His
 221 165 170 175
 222 ctc cgg gag cag atc cgc agc gag ttc acc ctg cac gac cac ctt cgg 576
 223 Leu Arg Glu Gln Ile Arg Ser Glu Phe Thr Leu His Asp His Leu Arg
 224 180 185 190
 225 caa gag gcc cag ggg gta ctg agt cag ttc cgt cta ccc cgc aca ggg 624
 226 Gln Glu Ala Gln Gly Val Leu Ser Gln Phe Arg Leu Pro Arg Thr Gly
 227 195 200 205
 228 gac cgc ccc agc acc ttc gtc ggg gtc cac gtc cgc cgc ggg gac tat 672
 229 Asp Arg Pro Ser Thr Phe Val Gly Val His Val Arg Arg Gly Asp Tyr
 230 210 215 220
 231 ctg cgt gtc atg ccc aag cgc tgg aag ggg gtc gtc ggt gac ggc gct 720
 232 Leu Arg Val Met Pro Lys Arg Trp Lys Gly Val Val Gly Asp Gly Ala
 233 225 230 235 240
 234 tac ctc cag cag gct atg gac tgg ttc cgg gcc cga tac gaa gcc ccc 768
 235 Tyr Leu Gln Gln Ala Met Asp Trp Phe Arg Ala Arg Tyr Glu Ala Pro
 236 245 250 255

RAW SEQUENCE LISTING . DATE: 11/20/2000
 PATENT APPLICATION: US/09/051,034A TIME: 12:18:28

Input Set : A:\305626u1.app
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253 gtc ttt gtg gtc acc aac ggc atg gag tgg tgc cgq aag aac atc 816
 254 Val Phe Val Val Thr Ser Asn Gly Met Glu Trp Cys Arg Lys Asn Ile
 255 260 265 270
 257 gac acc tcc cgg qgg gac gtg atc ttt qct ggc qat ggg cgg gag gcc 864
 258 Asp Thr Ser Arg Gly Asp Val Ile Phe Ala Gly Asp Gly Arg Glu Ala
 259 275 280 285
 261 qcq ccc qcc aqq gac ttt qcq ctq ctq qtq caq tyc aac cac acc atc 912
 262 Ala Pro Ala Arg Asp Phe Ala Leu Leu Val Gln Cys Asn His Thr Ile
 263 290 295 300
 265 alq acc att ggc acc ttc ggc ttc tgg gcc tac ctg gct ggt gga 960
 266 Met Thr Ile Gly Thr Phe Gly Phe Trp Ala Ala Tyr Leu Ala Gly Gly
 267 305 310 315 320
 269 qat acc atc tac ttq gct aac ttc acc ctg ccc act tcc agc ttc ctg 1008
 270 Asp Thr Ile Tyr Leu Ala Asn Phe Thr Leu Pro Thr Ser Ser Phe Leu
 271 325 330 335
 273 aaq atc ttt aaa ccc qaq gct qcc ttc ctg ccc qag tgg qtg ggc att 1056
 274 Lys Ile Phe Lys Pro Glu Ala Ala Phe Leu Pro Glu Trp Val Gly Ile
 275 340 345 350
 277 aat gca gac ttg tct cca ctc cag atg ttg gct ggg cct tga 1098
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 291 20 25 30
 292 Tyr Ser Gly Leu Asp Leu Leu Ala Leu Cys Pro Asp His Asn Val Val
 293 35 40 45
 294 Ser Ser Pro Val Ala Ile Phe Cys Leu Ala Gly Thr Pro Val His Pro
 295 50 55 60
 296 Asn Ala Ser Asp Ser Cys Pro Lys His Pro Ala Ser Phe Ser Gly Thr
 297 65 70 75 80
 298 Trp Thr Ile Tyr Pro Asp Gly Arg Phe Gly Asn Gln Met Gly Gln Tyr
 299 85 90 95
 300 Ala Thr Leu Ala Leu Ala Gln Leu Asn Gly Arg Gln Ala Phe Ile
 301 100 105 110
 302 Gln Pro Ala Met His Ala Val Leu Ala Pro Val Phe Arg Ile Thr Leu
 303 115 120 125
 304 Pro Val Leu Ala Pro Glu Val Asp Arg His Ala Pro Trp Arg Glu Leu
 305 130 135 140
 306 Glu Leu His Asp Trp Met Ser Glu Asp Tyr Ala His Leu Lys Glu Pro
 307 145 150 155 160
 308 Trp Leu Lys Leu Thr Gly Phe Pro Cys Ser Trp Thr Phe Phe His His
 309 165 170 175
 310 Leu Arg Glu Gln Ile Arg Ser Glu Phe Thr Leu His Asp His Leu Arg

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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/051,034A

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